FIGURE 14B

21/32

BURACASANZZOHOCHUCO > Z > O H O X H O X > E X A > H OUZURIANOKOKULERUZOR FIKMLTTFKTRAMPMFYSP HGRACPHGKARGGCOCHAG ONEXONNAKANACALAM ほしRVVLNFBPARMCGLOTO SHISHKHKHKIOKHUFOFO **しきよりとよりとのまんこうにっているよう** DOSTERNOSOFMACESHEDSS D II D A H I A D II > L A O I X H A D D D してくたいけららとじられりまただよりじら **VERTURE PARKEOUTO PALK** A CO B KO D SHK H Z L H L C L C L D レンソヨロソンひNAXPTILRLOL X J H H J > A O O > A X X Z Z F H R D 141 161 161 161 201 201 201 301 301

vertical bars indicate S.E.M. Data are presented as percent maximum cAMP r leased by 5-HT (basal cAMP rel ase: 0.023 ± 0.004 pmol/ml/10 min; maximum cAMP release: 0.57 ± 0.04 pmol/ml/10 min).

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Figure 11A: Nucleotide sequence of the partial human S10-87 clone. Only partial 3' untranslated sequences are shown (SEQ. ID NO. 14).

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Figure 11B: Deduced amino acid sequence encoded by the nucleotide sequence of Figure 11A of the partial human S10-87 clone (SEQ. ID NO. 15).

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Figure 12: Comparison of the nucleotide sequences between the human (top row) and the rat S10-87 (bottom row) cDNA clones. The overall identity is 90.8%.

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Figure 13: Comparison of the deduced amino acid sequences between the human (top row) and the rat (bottom row) S10-87 receptors. The overall identity is 93.9%.

Figure 14A: Nucleotide sequence of the full length human S10-95 clone (SEQ. ID NO. 7).

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Figure 14B: Deduced amino acid sequence encoded by the nucleotide sequence of Figure 14A (SEQ. ID NO. 8).

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rigure 15: Comparison of the nucleotide sequences between the human (top row) and the rat (bottom row) \$10-95 cDNA clones. The overall identity is 90.7%.

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Figure 16: Comparison of the deduced amino acid sequences between the human (top row) and the rat (bottom row) S10-95 receptors. The overall identity is 93.8%.